

1/32

## SEQUENCE LISTING

<110> Takeda Chemical Industries, Ltd.

<120> Novel Protein and its DNA

<130> 2568W00P

<150> JP 10-323759

<151> 1998-11-13

<150> JP 11-060030

<151> 1999-03-08

<150> JP 11-106812

<151> 1999-04-14

<150> JP 11-166672

<151> 1999-06-14

<150> JP 11-221640

<151> 1999-08-04

<150> JP 11-259818

<151> 1999-09-14

<160> 58

<210> 1

<211> 180

2/32

<212> PRT

<213> Human

<400> 1

Met Glu Ile Ile Ser Ser Lys Leu Phe Ile Leu Leu Thr Leu Ala Thr  
1 5 10 15  
Ser Ser Leu Leu Thr Ser Asn Ile Phe Cys Ala Asp Glu Leu Val Met  
20 25 30  
Ser Asn Leu His Ser Lys Glu Asn Tyr Asp Lys Tyr Ser Glu Pro Arg  
35 40 45  
Gly Tyr Pro Lys Gly Glu Arg Ser Leu Asn Phe Glu Glu Leu Lys Asp  
50 55 60  
Trp Gly Pro Lys Asn Val Ile Lys Met Ser Thr Pro Ala Val Asn Lys  
65 70 75 80  
Met Pro His Ser Phe Ala Asn Leu Pro Leu Arg Phe Gly Arg Asn Val  
85 90 95  
Gln Glu Glu Arg Ser Ala Gly Ala Thr Ala Asn Leu Pro Leu Arg Ser  
100 105 110  
Gly Arg Asn Met Glu Val Ser Leu Val Arg Arg Val Pro Asn Leu Pro  
115 120 125  
Gln Arg Phe Gly Arg Thr Thr Thr Ala Lys Ser Val Cys Arg Met Leu  
130 135 140  
Ser Asp Leu Cys Gln Gly Ser Met His Ser Pro Cys Ala Asn Asp Leu  
145 150 155 160  
Phe Tyr Ser Met Thr Cys Gln His Gln Glu Ile Gln Asn Pro Asp Gln  
165 170 175  
Lys Gln Ser Arg  
180

3/32

<210> 2

<211> 540

<212> DNA

<213> Human

<400> 2

ATGGAAATTA TTTCATCAAA ACTATTCATT TTATTGACTT TAGCCACTTC AAGCTTGTTA 60  
 ACATCAAACA TTTTGTGTC AGATGAATTA GTGATGTCCA ATCTTCACAG CAAAGAAAAT 120  
 TATGACAAAT ATTCTGAGCC TAGAGGATAC CCAAAAGGGG AAAGAAGCCT CAATTTTGAG 180  
 GAATTA AAAAG ATTGGGGACC AAAAAATGTT ATTAAGATGA GTACACCTGC AGTCAATAAA 240  
 ATGCCACACT CCTTCGCCAA CTTGCCATTG AGATTTGGGA GGAACGTTCA AGAAGAAAGA 300  
 AGTGCTGGAG CAACAGCCAA CCTGCCTCTG AGATCTGGA AGAAATATGGA GGTGAGCCTC 360  
 GTGAGACGTG TTCCTAACCT GCCCCAAAGG TTTGGGAGAA CAACAACAGC CAAAAGTGTC 420  
 TGCAGGATGC TGAGTGATTT GTGTCAAGGA TCCATGCATT CACCATGTGC CAATGACTTA 480  
 TTTTACTCCA TGACCTGCCA GCACCAAGAA ATCCAGAATC CCGATCAAAA ACAGTCAAGG 540

<210> 3

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223>

<400> 3

GGGCTGCACA TAGAGACTTA ATTTTAG 27

<210> 4

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

4/32

&lt;223&gt;

&lt;400&gt; 4

CTAGACCACC TCTATATAAC TGCCCAT

27

&lt;210&gt; 5

&lt;211&gt; 30

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt;

&lt;400&gt; 5

GCACATAGAG ACTTAATTTT AGATTTAGAC

30

&lt;210&gt; 6

&lt;211&gt; 27

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt;

&lt;400&gt; 6

CATGCACTTT GACTGGTTTC CAGGTAT

27

&lt;210&gt; 7

&lt;211&gt; 27

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt;

&lt;400&gt; 7

CAGCTTTAGG GACAGGCTCC AGGTTTC

27

5/32

&lt;210&gt; 8

&lt;211&gt; 196

&lt;212&gt; PRT

&lt;213&gt; Human

&lt;400&gt; 8

Met Glu Ile Ile Ser Ser Lys Leu Phe Ile Leu Leu Thr Leu Ala Thr  
 1 5 10 15  
 Ser Ser Leu Leu Thr Ser Asn Ile Phe Cys Ala Asp Glu Leu Val Met  
 20 25 30  
 Ser Asn Leu His Ser Lys Glu Asn Tyr Asp Lys Tyr Ser Glu Pro Arg  
 35 40 45  
 Gly Tyr Pro Lys Gly Glu Arg Ser Leu Asn Phe Glu Glu Leu Lys Asp  
 50 55 60  
 Trp Gly Pro Lys Asn Val Ile Lys Met Ser Thr Pro Ala Val Asn Lys  
 65 70 75 80  
 Met Pro His Ser Phe Ala Asn Leu Pro Leu Arg Phe Gly Arg Asn Val  
 85 90 95  
 Gln Glu Glu Arg Ser Ala Gly Ala Thr Ala Asn Leu Pro Leu Arg Ser  
 100 105 110  
 Gly Arg Asn Met Glu Val Ser Leu Val Arg Arg Val Pro Asn Leu Pro  
 115 120 125  
 Gln Arg Phe Gly Arg Thr Thr Thr Ala Lys Ser Val Cys Arg Met Leu  
 130 135 140  
 Ser Asp Leu Cys Gln Gly Ser Met His Ser Pro Cys Ala Asn Asp Leu  
 145 150 155 160  
 Phe Tyr Ser Met Thr Cys Gln His Gln Glu Ile Gln Asn Pro Asp Gln  
 165 170 175

6/32

Lys Gln Ser Arg Arg Leu Leu Phe Lys Lys Ile Asp Asp Ala Glu Leu

180

185

190

Lys Gln Glu Lys

195

&lt;210&gt; 9

&lt;211&gt; 588

&lt;212&gt; DNA

&lt;213&gt; Human

&lt;400&gt; 9

ATGGAAATTA TTTCATCAAA ACTATTCATT TTATTGACTT TAGCCACTTC AAGCTTGTTA 60

ACATCAAACA TTTTGTGTC AGATGAATTA GTGATGTCCA ATCTTCACAG CAAAGAAAAT 120

TATGACAAAT ATTCTGAGCC TAGAGGATAC CAAAAGGGG AAAGAAGCCT CAATTTTGAG 180

GAATTAAAAG ATTGGGGACC AAAAAATGTT ATTAAGATGA GTACACCTGC AGTCAATAAA 240

ATGCCACACT CCTTCGCCAA CTGCCATTG AGATTTGGGA GGAACGTTCA AGAAGAAAGA 300

AGTGCTGGAG CAACAGCCAA CCTGCCTCTG AGATCTGGAA GAAATATGGA GGTGAGCCTC 360

GTGAGACGTG TTCCTAACCT GCCCAAAGG TTTGGGAGAA CAACAACAGC CAAAAGTGTC 420

TGCAGGATGC TGAGTGATTT GTGTCAAGGA TCCATGCATT CACCATGTGC CAATGACTTA 480

TTTACTCCA TGACCTGCCA GCACCAAGAA ATCCAGAATC CCGATCAAAA ACAGTCAAGG 540

AGACTGCTAT TCAAGAAAAT AGATGATGCA GAATTGAAAC AAGAAAAA 588

&lt;210&gt; 10

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223>

<400> 10

GCCTAGAGGA GATCTAGGCT GGGAGGA

27

<210> 11

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223>

<400> 11

GGGAGGAACA TGGAAGAAGA AAGGAGC

27

<210> 12

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223>

<400> 12

GATGGTGAAT GCATGGACTG CTGGAGC

27

<210> 13

<211> 27

<212> DNA

<213> Artificial Sequence

8/32

&lt;220&gt;

&lt;223&gt;

&lt;400&gt; 13

TTCCTCCCAA ATCTCAGTGG CAGGTTG

27

&lt;210&gt; 14

&lt;211&gt; 196

&lt;212&gt; PRT.

&lt;213&gt; Bovine

&lt;400&gt; 14

Met Glu Ile Ile Ser Leu Lys Arg Phe Ile Leu Leu Met Leu Ala Thr

1 5 10 15

Ser Ser Leu Leu Thr Ser Asn Ile Phe Cys Thr Asp Glu Ser Arg Met

20 25 30

Pro Asn Leu Tyr Ser Lys Lys Asn Tyr Asp Lys Tyr Ser Glu Pro Arg

35 40 45

Gly Asp Leu Gly Trp Glu Lys Glu Arg Ser Leu Thr Phe Glu Glu Val

50 55 60

Lys Asp Trp Ala Pro Lys Ile Lys Met Asn Lys Pro Val Val Asn Lys

65 70 75 80

Met Pro Pro Ser Ala Ala Asn Leu Pro Leu Arg Phe Gly Arg Asn Met

85 90 95

Glu Glu Glu Arg Ser Thr Arg Ala Met Ala His Leu Pro Leu Arg Leu

100 105 110

Gly Lys Asn Arg Glu Asp Ser Leu Ser Arg Trp Val Pro Asn Leu Pro

115 120 125

Gln Arg Phe Gly Arg Thr Thr Thr Ala Lys Ser Ile Thr Lys Thr Leu

130 135 140



9/32

Ser Asn Leu Leu Gln Gln Ser Met His Ser Pro Ser Thr Asn Gly Leu  
 145                      150                      155                      160  
 Leu Tyr Ser Met Ala Cys Gln Pro Gln Glu Ile Gln Asn Pro Gly Gln  
                     165                      170                      175  
 Lys Asn Leu Arg Arg Arg Gly Phe Gln Lys Ile Asp Asp Ala Glu Leu  
                     180                      185                      190  
 Lys Gln Glu Lys

195

<210> 15  
 <211> 588  
 <212> DNA  
 <213> Bovine  
 <400> 15  
 <210> 15  
 <211> 588  
 <212> DNA  
 <213> Bovine

<400> 15

ATGGAAATTA TTTCATTAAA ACGATTCATT TTATTGATGT TAGCCACTTC AAGCTTGTTA 60  
 ACATCAAACA TCTTCTGCAC AGACGAATCA AGGATGCCCA ATCTTTACAG CAAAAAGAAT 120  
 TATGACAAAT ATTCCGAGCC TAGAGGAGAT CTAGGCTGGG AGAAAGAAAG AAGTCTTACT 180  
 TTTGAAGAAG TAAAAGATTG GGCTCCAAAA ATTAAGATGA ATAAACCTGT AGTCAACAAA 240  
 ATGCCACCTT CTGCAGCCAA CCTGCCACTG AGATTGTTGGA GGAACATGGA AGAAGAAAGG 300

<212> PRT

26

11/32

&lt;213&gt; Rat

&lt;400&gt; 18

Met Glu Ile Ile Ser Ser Lys Arg Phe Ile Leu Leu Thr Leu Ala Thr

1 5 10 15

Ser Ser Phe Leu Thr Ser Asn Thr Leu Cys Ser Asp Glu Leu Met Met

20 25 30

Pro His Phe His Ser Lys Glu Gly Tyr Gly Lys Tyr Tyr Gln Leu Arg

35 40 45

Gly Ile Pro Lys Gly Val Lys Glu Arg Ser Val Thr Phe Gln Glu Leu

50 55 60

Lys Asp Trp Gly Ala Lys Lys Asp Ile Lys Met Ser Pro Ala Pro Ala

65 70 75 80

Asn Lys Val Pro His Ser Ala Ala Asn Leu Pro Leu Arg Phe Gly Arg

85 90 95

Asn Ile Glu Asp Arg Arg Ser Pro Arg Ala Arg Ala Asn Met Glu Ala

100 105 110

Gly Thr Met Ser His Phe Pro Ser Leu Pro Gln Arg Phe Gly Arg Thr

115 120 125

Thr Ala Arg Arg Ile Thr Lys Thr Leu Ala Gly Leu Pro Gln Lys Ser

130 135 140

Leu His Ser Leu Ala Ser Ser Glu Ser Leu Tyr Ala Met Thr Arg Gln

145 150 155 160

His Gln Glu Ile Gln Ser Pro Gly Gln Glu Gln Pro Arg Lys Arg Val

165 170 175

Phe Thr Glu Thr Asp Asp Ala Glu Arg Lys Gln Glu Lys Ile Gly Asn

180 185 190

200

<400> 20

13/32

12

MGNTTYGGNA AR

&lt;210&gt; 21

&lt;211&gt; 12

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt;

&lt;400&gt; 21

12

MGNTTYGGNM GN

&lt;210&gt; 22

&lt;211&gt; 12

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt;

&lt;400&gt; 22

12

MGNWSNGGNA AR

&lt;210&gt; 23

&lt;211&gt; 12

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt;

&lt;400&gt; 23

12

MGNWSNGGNM GN

&lt;210&gt; 24

&lt;211&gt; 12

<212> DNA

<213> Artificial Sequence

<220>

<223>

<400> 24

12

MGNYTNGGNA AR

<210> 25

<211> 12

<212> DNA

<213> Artificial Sequence

<220>

<223>

<400> 25

12

MGNYTNGGNM GN

<210> 26

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223>

<400> 26

30

GACTTAATTT TAGATTAGA CAAAATGGAA

<210> 27

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223>

<400> 27

TTCTCCCAA CCTTTGGGGC AGGTT

25

<210> 28

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223>

<400> 28

ACAGCAAAGA AGGTGACGGA AAATACTC

28

<210> 29

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223>

<400> 29

ATAGATGAGA AAAGAAGCCC CGCAGCAC

28

<210> 30

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

16/32

&lt;223&gt;

&lt;400&gt; 30

GTGCTGCGGG GCTTCTTTTC TCATCTAT

28

&lt;210&gt; 31

&lt;211&gt; 21

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt;

&lt;400&gt; 31

TTTAGACTTA GACGAAATGG A

21

&lt;210&gt; 32

&lt;211&gt; 21

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt;

&lt;400&gt; 32

GCTCCGTAGC CTCTTGAAGT C

21

&lt;210&gt; 33

&lt;211&gt; 188

&lt;212&gt; PRT

&lt;213&gt; Mouse

&lt;400&gt; 33



17/32

Met Glu Ile Ile Ser Leu Lys Arg Phe Ile Leu Leu Thr Val Ala Thr  
 1 5 10 15  
 Ser Ser Phe Leu Thr Ser Asn Thr Phe Cys Thr Asp Glu Phe Met Met  
 20 25 30  
 Pro His Phe His Ser Lys Glu Gly Asp Gly Lys Tyr Ser Gln Leu Arg  
 35 40 45  
 Gly Ile Pro Lys Gly Glu Lys Glu Arg Ser Val Ser Phe Gln Glu Leu  
 50 55 60  
 Lys Asp Trp Gly Ala Lys Asn Val Ile Lys Met Ser Pro Ala Pro Ala  
 65 70 75 80  
 Asn Lys Val Pro His Ser Ala Ala Asn Leu Pro Leu Arg Phe Gly Arg  
 85 90 95  
 Thr Ile Asp Glu Lys Arg Ser Pro Ala Ala Arg Val Asn Met Glu Ala  
 100 105 110  
 Gly Thr Arg Ser His Phe Pro Ser Leu Pro Gln Arg Phe Gly Arg Thr  
 115 120 125  
 Thr Ala Arg Ser Pro Lys Thr Pro Ala Asp Leu Pro Gln Lys Pro Leu  
 130 135 140  
 His Ser Leu Gly Ser Ser Glu Leu Leu Tyr Val Met Ile Cys Gln His  
 145 150 155 160  
 Gln Glu Ile Gln Ser Pro Gly Gly Lys Arg Thr Arg Arg Gly Ala Phe  
 165 170 175  
 Val Glu Thr Asp Asp Ala Glu Arg Lys Pro Glu Lys  
 180 185

&lt;210&gt; 34

&lt;211&gt; 564

18/32

&lt;212&gt; DNA

&lt;213&gt; Mouse

&lt;400&gt; 34

ATGGAAATTA TTTCATTAAA ACGATTCATT TTATTGACTG TGGCAACTTC AAGCTTCTTA 60  
 ACATCAAACA CCTTCTGTAC AGATGAGTTC ATGATGCCTC ATTTTCACAG CAAAGAAGGT 120  
 GACGGAAAAT ACTCCCAGCT GAGAGGAATC CAAAAGGGG AAAAGGAAAG AAGTGTCAGT 180  
 TTTCAAGAAC TAAAAGATTG GGGGGCAAAG AATGTTATTA AGATGAGTCC AGCCCCTGCC 240  
 AACAAAGTGC CCCACTCAGC AGCCAACCTG CCCCTGAGAT TTGGAAGGAC CATAGATGAG 300  
 AAAAGAAGCC CCGCAGCAGC GGTCAACATG GAGGCAGGGA CCAGGAGCCA TTTCCCCAGC 360  
 CTGCCCCAAA GGTTTGGGAG AACAACAGCC AGAAGCCCCA AGACACCCGC TGATTTGCCA 420  
 CAGAAACCCC TGCACTCACT GGGCTCCAGC GAGTTGCTCT ACGTCATGAT CTGCCAGCAC 480  
 CAAGAAATTC AGAGTCCTGG TGGAAAGCGA ACGAGGAGAG GAGCGTTTGT GGAAACAGAT 540  
 GATGCAGAAA GGAAACCAGA AAAA 564

&lt;210&gt; 35

&lt;211&gt; 27

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt;

&lt;400&gt; 35

AGTCGACAGT ATGGAGGCGG AGCCCTC

27

&lt;210&gt; 36

&lt;211&gt; 29

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

$\langle 220 \rangle$ 

<223>

<400> 36

GACTAGTTCA AATGTTCCAG GCCGGGATG

29

<210> 37

$\langle 211 \rangle$  432

&lt;212&gt; PRT

<213> Rat

<400> 37

Met Glu Ala Glu Pro Ser Gln Pro Pro Asn Gly Ser Trp Pro Leu Gly

				5					10					15			
Gln	Asn	Gly	Ser	Asp	Val	Glu	Thr	Ser	Met	Ala	Thr	Ser	Leu	Thr	Phe		
			20					25					30				
Ser	Ser	Tyr	Tyr	Gln	His	Ser	Ser	Pro	Val	Ala	Ala	Met	Phe	Ile	Ala		
		35					40					45					
Ala	Tyr	Val	Leu	Ile	Phe	Leu	Leu	Cys	Met	Val	Gly	Asn	Thr	Leu	Val		
	50					55					60						
Cys	Phe	Ile	Val	Leu	Lys	Asn	Arg	His	Met	Arg	Thr	Val	Thr	Asn	Met		
65					70					75					80		
Phe	Ile	Leu	Asn	Leu	Ala	Val	Ser	Asp	Leu	Leu	Val	Gly	Ile	Phe	Cys		
			85						90					95			
Met	Pro	Thr	Thr	Leu	Val	Asp	Asn	Leu	Ile	Thr	Gly	Trp	Pro	Phe	Asp		
			100					105					110				
Asn	Ala	Thr	Cys	Lys	Met	Ser	Gly	Leu	Val	Gln	Gly	Met	Ser	Val	Ser		
		115					120					125					
Ala	Ser	Val	Phe	Thr	Leu	Val	Ala	Ile	Ala	Val	Glu	Arg	Phe	Arg	Cys		
	130					135					140						
Ile	Val	His	Pro	Phe	Arg	Glu	Lys	Leu	Thr	Leu	Arg	Lys	Ala	Leu	Phe		
145					150					155					160		
Thr	Ile	Ala	Val	Ile	Trp	Ala	Leu	Ala	Leu	Leu	Ile	Met	Cys	Pro	Ser		
				165				170						175			
Ala	Val	Thr	Leu	Thr	Val	Thr	Arg	Glu	Glu	His	His	Phe	Met	Leu	Asp		
			180					185					190				
Ala	Arg	Asn	Arg	Ser	Tyr	Pro	Leu	Tyr	Ser	Cys	Trp	Glu	Ala	Trp	Pro		

20/32

195	200	205
Glu Lys Gly Met Arg Lys Val Tyr Thr Ala Val Leu Phe Ala His Ile		
210	215	220
Tyr Leu Val Pro Leu Ala Leu Ile Val Val Met Tyr Val Arg Ile Ala		
225	230	235
Arg Lys Leu Cys Gln Ala Pro Gly Pro Ala Arg Asp Thr Glu Glu Ala		240
	245	250
Val Ala Glu Gly Gly Arg Thr Ser Arg Arg Arg Ala Arg Val Val His		255
	260	265
Met Leu Val Met Val Ala Leu Phe Phe Thr Leu Ser Trp Leu Pro Leu		270
	275	280
Trp Val Leu Leu Leu Leu Ile Asp Tyr Gly Glu Leu Ser Glu Leu Gln		285
	290	295
Leu His Leu Leu Ser Val Tyr Ala Phe Pro Leu Ala His Trp Leu Ala		300
305	310	315
Phe Phe His Ser Ser Ala Asn Pro Ile Ile Tyr Gly Tyr Phe Asn Glu		320
	325	330
Asn Phe Arg Arg Gly Phe Gln Ala Ala Phe Arg Ala Gln Leu Cys Trp		335
	340	345
Pro Pro Trp Ala Ala His Lys Gln Ala Tyr Ser Glu Arg Pro Asn Arg		350
	355	360
Leu Leu Arg Arg Arg Val Val Val Asp Val Gln Pro Ser Asp Ser Gly		365
	370	375
Leu Pro Ser Glu Ser Gly Pro Ser Ser Gly Val Pro Gly Pro Gly Arg		380
385	390	395
Leu Pro Leu Arg Asn Gly Arg Val Ala His Gln Asp Gly Pro Gly Glu		400
	405	410
Gly Pro Gly Cys Asn His Met Pro Leu Thr Ile Pro Ala Trp Asn Ile		415
	420	425
		430

&lt;210&gt; 38

&lt;211&gt; 1299

&lt;212&gt; DNA

&lt;213&gt; Rat

&lt;400&gt; 38

ATGGAGGCGG AGCCCTCCCA GCCTCCCAAC GGCAGCTGGC CCCTGGGTCA GAACGGGAGT 60

GATGTGGAGA CCAGCATGGC AACCAGCCTC ACCTTCTCCT CCTACTACCA AACTCCTCT 120

CCGGTGGCAG CCATGTTTAT CGCGGCCTAC GTGCTCATCT TCCTCCTCTG CATGGTGGGC 180

21/32

AACACCCTGG TCTGCTTCAT TGTGCTCAAG AACCGGCACA TGC GCACTGT CACCAACATG 240  
 TTTATCCTCA ACCTGGCCGT CAGCGACCTG CTGGTGGGCA TCTTCTGCAT GCCCACAACC 300  
 CTTGTGGACA ACCTTATCAC TGGTTGGCCT TTTGACAACG CCACATGCAA GATGAGCGGC 360  
 TTGGTGCAGG GCATGTCCGT GTCTGCATCG GTTTTACAC TGGTGGCCAT CGCTGTGGAA 420  
 AGGTTCCGCT GCATCGTGCA CCCTTTCCGC GAGAAGCTGA CCCTTCGGAA GGCGCTGTTC 480  
 ACCATCGCGG TGATCTGGGC TCTGGCGCTG CTCATCATGT GTCCCTCGGC GGTCACCTCTG 540  
 ACAGTCACCC GAGAGGAGCA TCACTTCATG CTGGATGCTC GTAACCGCTC CTACCCGCTC 600  
 TACTCGTGCT GGGAGGCCTG GCCCAGAGAAG GGCATGCGCA AGGTCTACAC CGCGGTGCTC 660  
 TTCGCGCACA TCTACCTGGT GCCGCTGGCG CTCATCGTAG TGATGTACGT GCGCATCGCG 720  
 CGCAAGCTAT GCCAGGCCCC CGGTCCTGCG CGCGACACGG AGGAGGCGGT GGCCGAGGGT 780  
 GGCCGCACTT CGCGCCGTAG GGCCCGCGTG GTGCACATGC TGGTCATGGT GGCGCTCTTC 840  
 TTCACGTTGT CCTGGCTGCC ACTCTGGGTG CTGCTGCTGC TCATCGACTA TGGGGAGCTG 900  
 AGCGAGCTGC AACTGCACCT GCTGTGGTTC TACGCCTTCC CCTTGGCACA CTGGCTGGCC 960  
 TTCTTCCACA GCAGCGCCAA CCCCATCATC TACGGCTACT TCAACGAGAA CTTCCGCCGC 1020  
 GGCTTCCAGG CTGCCTTCCG TGCACAGCTC TGCTGGCCTC CCTGGGCCGC CCACAAGCAA 1080  
 GCCTACTCGG AGCGGCCCAA CCGCCTCCTG CGCAGGCGGG TGGTGGTGGA CGTGCAACCC 1140  
 AGCGACTCCG GCCTGCCATC AGAGTCTGGC CCCAGCAGCG GGGTCCCAGG GCCTGGCCGG 1200  
 CTGCCACTGC GCAATGGGCG TGTGGCCCAT CAGGATGGCC CGGGGAAGG GCCAGGCTGC 1260  
 AACCATATGC CCCTCACCAT CCCGGCCTGG AACATTTGA 1299

<210> 39

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> the C-terminus of the polypeptide is amide (-CONH<sub>2</sub>) form

22/32

&lt;400&gt; 39

Met Pro His Ser Phe Ala Asn Leu Pro Leu Arg Phe  
1 5 10

&lt;210&gt; 40

&lt;211&gt; 8

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> the C-terminus of the polypeptide is amide (-CONH<sub>2</sub>) form

&lt;400&gt; 40

Val Pro Asn Leu Pro Gln Arg Phe

1 5

&lt;210&gt; 41

&lt;211&gt; 11

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> the C-terminus of the polypeptide is amide (-CONH<sub>2</sub>) form

&lt;400&gt; 41

Ser Ala Gly Ala Thr Ala Asn Leu Pro Arg Ser

1 5 10

&lt;210&gt; 42

&lt;211&gt; 36

&lt;212&gt; DNA

&lt;213&gt; Human

&lt;400&gt; 42

23/32

ATGCCACACT CCTTCGCCAA CTTGCCATTG AGATT

36

&lt;210&gt; 43

&lt;211&gt; 36

&lt;212&gt; DNA

&lt;213&gt; Human

&lt;400&gt; 43

AGTGCTGGAG CAACAGCCAA CCTGCCTCTG AGATCT

36

&lt;210&gt; 44

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Human

&lt;400&gt; 44

GTTCTAACC TGCCCCAAAG GTTT

24

&lt;210&gt; 45

&lt;211&gt; 276

&lt;212&gt; DNA

&lt;213&gt; Human

&lt;400&gt; 45

ATGGAAATTA TTTCATCAAA ACTATTCATT TTATTGACTT TAGCCACTTC AAGCTTGTTA 60

ACATCAAACA TTTTGTGTC AGATGAATTA GTGATGTCCA ATCTTCACAG CAAAGAAAAT 120

TATGACAAAT ATTCTGAGCC TAGAGGATAC CAAAAGGGG AAAGAAGCCT CAATTTTGAG 180

GAATTAAAAG ATTGGGGACC AAAAAATGTT ATTAAGATGA GTACACCTGC AGTCAATAAA 240

ATGCCACACT CCTTCGCCAA CTTGCCATTG AGATT 276

&lt;210&gt; 46

&lt;211&gt; 336

&lt;212&gt; DNA

&lt;213&gt; Human

24/32

&lt;400&gt; 46

ATGGAAATTA TTTCATCAAA ACTATTCATT TTATTGACTT TAGCCACTTC AAGCTTGTTA 60  
 ACATCAAACA TTTTGTGTC AGATGAATTA GTGATGTCCA ATCTTCACAG CAAAGAAAAT 120  
 TATGACAAAT ATTCTGAGCC TAGAGGATAC CCAAAGGGG AAAGAAGCCT CAATTTTGAG 180  
 GAATTAAAAG ATTGGGGACC AAAAAATGTT ATTAAGATGA GTACACCTGC AGTCAATAAA 240  
 ATGCCACACT CCTTCGCCAA CTTGCCATTG AGATTTGGGA GGAACGTTCA AGAAGAAAGA 300  
 AGTGCTGGAG CAACAGCCAA CCTGCCTCTG AGATCT 336

&lt;210&gt; 47

&lt;211&gt; 393

&lt;212&gt; DNA

&lt;213&gt; Human

&lt;400&gt; 47

ATGGAAATTA TTTCATCAAA ACTATTCATT TTATTGACTT TAGCCACTTC AAGCTTGTTA 60  
 ACATCAAACA TTTTGTGTC AGATGAATTA GTGATGTCCA ATCTTCACAG CAAAGAAAAT 120  
 TATGACAAAT ATTCTGAGCC TAGAGGATAC CCAAAGGGG AAAGAAGCCT CAATTTTGAG 180  
 GAATTAAAAG ATTGGGGACC AAAAAATGTT ATTAAGATGA GTACACCTGC AGTCAATAAA 240  
 ATGCCACACT CCTTCGCCAA CTTGCCATTG AGATTTGGGA GGAACGTTCA AGAAGAAAGA 300  
 AGTGCTGGAG CAACAGCCAA CCTGCCTCTG AGATCTGGA AGAAATATGGA GGTGAGCCTC 360  
 GTGAGACGTG TTCCTAACCT GCCCAAAGG TTT 393

&lt;210&gt; 48

&lt;211&gt; 27

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt;

&lt;400&gt; 48



25/32

CCCTGGGGCT TCTTCTGTCT TCTATGT

27

&lt;210&gt; 49

&lt;211&gt; 26

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt;

&lt;400&gt; 49

AGCGATTCAT TTTATTGACT TTAGCA

26

&lt;210&gt; 50

&lt;211&gt; 203

&lt;212&gt; PRT

&lt;213&gt; Rat

&lt;400&gt; 50

Met Glu Ile Ile Ser Ser Lys Arg Phe Ile Leu Leu Thr Leu Ala Thr

1 5 10 15

Ser Ser Phe Leu Thr Ser Asn Thr Leu Cys Ser Asp Glu Leu Met Met

20 25 30

Pro His Phe His Ser Lys Glu Gly Tyr Gly Lys Tyr Tyr Gln Leu Arg

35 40 45

Gly Ile Pro Lys Gly Val Lys Glu Arg Ser Val Thr Phe Gln Glu Leu

50 55 60

Lys Asp Trp Gly Ala Lys Lys Asp Ile Lys Met Ser Pro Ala Pro Ala

65 70 75 80

Asn Lys Val Pro His Ser Ala Ala Asn Leu Pro Leu Arg Phe Gly Arg

26/32

	85	90	95
Asn Ile Glu Asp Arg Arg Ser Pro Arg Ala Arg Ala Asn Met Glu Ala			
100	105	110	
Gly Thr Met Ser His Phe Pro Ser Leu Pro Gln Arg Phe Gly Arg Thr			
115	120	125	
Thr Ala Arg Arg Ile Thr Lys Thr Leu Ala Gly Leu Pro Gln Lys Ser			
130	135	140	
Leu His Ser Leu Ala Ser Ser Glu Leu Leu Tyr Ala Met Thr Arg Gln			
145	150	155	160
His Gln Glu Ile Gln Ser Pro Gly Gln Glu Gln Pro Arg Lys Arg Val			
165	170	175	
Phe Thr Glu Thr Asp Asp Ala Glu Arg Lys Gln Glu Lys Ile Gly Asn			
180	185	190	
Leu Gln Pro Val Leu Gln Gly Ala Met Lys Leu			
195	200		

&lt;210&gt; 51

&lt;211&gt; 609

&lt;212&gt; DNA

&lt;213&gt; Rat

&lt;400&gt; 51

ATGGAAATTA TTTCATCAAA GCGATTCATT TTATTGACTT TAGCAACTTC AAGCTTCTTA	60
ACTTCAAACA CCCTTTGTTC AGATGAATTA ATGATGCCCC ATTTTCACAG CAAAGAAGGT	120
TATGGAAAAT ATTACCAGCT GAGAGGAATC CCAAAAGGGG TAAAGGAAAG AAGTGTCAC	180
TTTCAAGAAC TCAAAGATTG GGGGGCAAAG AAAGATATTA AGATGAGTCC AGCCCCTGCC	240
AACAAAGTGC CCCACTCAGC AGCCAACCTT CCCCTGAGGT TTGGGAGGAA CATAGAAGAC	300

&lt;212&gt; PRT

28/32

&lt;213&gt; Human

&lt;400&gt; 54

Met Glu Gly Glu Pro Ser Gln Pro Pro Asn Ser Ser Trp Pro Leu Ser

1 5 10 15

Gln Asn Gly Thr Asn Thr Glu Ala Thr Pro Ala Thr Asn Leu Thr Phe

20 25 30

Ser Ser Tyr Tyr Gln His Thr Ser Pro Val Ala Ala Met Phe Ile Val

35 40 45

Ala Tyr Ala Leu Ile Phe Leu Leu Cys Met Val Gly Asn Thr Leu Val

50 55 60

Cys Phe Ile Val Leu Lys Asn Arg His Met His Thr Val Thr Asn Met

65 70 75 80

Phe Ile Leu Asn Leu Ala Val Ser Asp Leu Leu Val Gly Ile Phe Cys

85 90 95

Met Pro Thr Thr Leu Val Asp Asn Leu Ile Thr Gly Trp Pro Phe Asp

100 105 110

Asn Ala Thr Cys Lys Met Ser Gly Leu Val Gln Gly Met Ser Val Ser

115 120 125

Ala Ser Val Phe Thr Leu Val Ala Ile Ala Val Glu Arg Phe Arg Cys

130 135 140

Ile Val His Pro Phe Arg Glu Lys Leu Thr Leu Arg Lys Ala Leu Val

145 150 155 160

Thr Ile Ala Val Ile Trp Ala Leu Ala Leu Leu Ile Met Cys Pro Ser

165 170 175

Ala Val Thr Leu Thr Val Thr Arg Glu Glu His His Phe Met Val Asp

180 185 190

Ala Arg Asn Arg Ser Tyr Pro Leu Tyr Ser Cys Trp Glu Ala Trp Pro

29/32

195	200	205
Glu Lys Gly Met Arg Arg Val Tyr Thr Thr Val Leu Phe Ser His Ile		
210	215	220
Tyr Leu Ala Pro Leu Ala Leu Ile Val Val Met Tyr Ala Arg Ile Ala		
225	230	235
Arg Lys Leu Cys Gln Ala Pro Gly Pro Ala Pro Gly Gly Glu Glu Ala		240
245	250	255
Ala Asp Pro Arg Ala Ser Arg Arg Arg Ala Arg Val Val His Met Leu		
260	265	270
Val Met Val Ala Leu Phe Phe Thr Leu Ser Trp Leu Pro Leu Trp Ala		
275	280	285
Leu Leu Leu Leu Ile Asp Tyr Gly Gln Leu Ser Ala Pro Gln Leu His		
290	295	300
Leu Val Thr Val Tyr Ala Phe Pro Phe Ala His Trp Leu Ala Phe Phe		
305	310	315
Asn Ser Ser Ala Asn Pro Ile Ile Tyr Gly Tyr Phe Asn Glu Asn Phe		320
325	330	335
Arg Arg Gly Phe Gln Ala Ala Phe Arg Ala Arg Leu Cys Pro Arg Pro		
340	345	350
Ser Gly Ser His Lys Glu Ala Tyr Ser Glu Arg Pro Gly Gly Leu Leu		
355	360	365
His Arg Arg Val Phe Val Val Val Arg Pro Ser Asp Ser Gly Leu Pro		
370	375	380
Ser Glu Ser Gly Pro Ser Ser Gly Ala Pro Arg Pro Gly Arg Leu Pro		
385	390	395
Leu Arg Asn Gly Arg Val Ala His His Gly Leu Pro Arg Glu Gly Pro		400
405	410	415

30/32

Gly Cys Ser His Leu Pro Leu Thr Ile Pro Ala Trp Asp Ile

420

425

430

&lt;210&gt; 55

&lt;211&gt; 1290

&lt;212&gt; DNA

&lt;213&gt; Human

&lt;400&gt; 55

ATGGAGGGGG AGCCCTCCCA GCCTCCCAAC AGCAGTTGGC CCCTAAGTCA GAATGGGACT 60  
 AACACTGAGG CCACCCCGGC TACAAACCTC ACCTTCTCCT CCTACTATCA GCACACCTCC 120  
 CCTGTGGCGG CCATGTTTCAT TGTGGCCTAT GCGCTCATCT TCCTGCTCTG CATGGTGGGC 180  
 AACACCCTGG TCTGTTTCAT CGTGCTCAAG AACCGGCACA TGCATACTGT CACCAACATG 240  
 TTCATCCTCA ACCTGGCTGT CAGTGACCTG CTGGTGGGCA TCTTCTGCAT GCCCACCACC 300  
 CTTGTGGACA ACCTCATCAC TGGGTGGCCC TTCGACAATG CCACATGCAA GATGAGCGGC 360  
 TTGGTGCAGG GCATGTCTGT GTCGGCTTCC GTTTTCACAC TGGTGGCCAT TGCTGTGGAA 420  
 AGGTTCCGCT GCATCGTGCA CCCTTTCCGC GAGAAGCTGA CCCTGCGGAA GCGCTCGTC 480  
 ACCATCGCCG TCATCTGGGC CCTGGCGCTG CTCATCATGT GTCCCTCGGC CGTCACGCTG 540  
 ACCGTCACCC GTGAGGAGCA CCACTTCATG GTGGACGCCC GCAACCGCTC CTACCCTCTC 600  
 TACTCCTGCT GGGAGGCCTG GCCCGAGAAG GGCATGCGCA GGGTCTACAC CACTGTGCTC 660  
 TTCTCGCACA TCTACCTGGC GCCGCTGGCG CTCATCGTGG TCATGTACGC CCGCATCGCG 720  
 CGCAAGCTCT GCCAGGCCCC GGGCCCGGCC CCCGGGGGCG AGGAGGCTGC GGACCCGCGA 780  
 GCATCGCGGC GCAGAGCGCG CGTGGTGCAC ATGCTGGTCA TGGTGGCGCT GTTCTTCACG 840  
 CTGTCCTGGC TGCCGCTCTG GCGGCTGCTG CTGCTCATCG ACTACGGGCA GCTCAGCGCG 900  
 CCGCAGCTGC ACCTGGTCAC CGTCTACGCC TTCCCCTTCG CGCACTGGCT GGCCTTCTTC 960  
 AACAGCAGCG CCAACCCCAT CATCTACGGC TACTTCAACG AGAACTTCCG CCGCGGCTTC 1020  
 CAGGCCGCCT TCCGCGCCCG CCTCTGCCCC CGCCCGTCGG GGAGCCACAA GGAGGCCTAC 1080  
 TCCGAGCGGC CCGGCGGGCT TCTGCACAGG CGGGTCTTCG TGGTGGTGCG GCCCAGCGAC 1140  
 TCCGGGCTGC CCTCTGAGTC GGGCCCTAGC AGTGGGGCCC CCAGGCCCGG CCGCCTCCCG 1200

31/32

CTGCGGAATG GGC GGGTGGC TCACCACGGC TTGCCCAGGG AAGGGCCTGG CTGCTCCCAC 1260  
 CTGCCCCTCA CCATTCCAGC CTGGGATATC 1290

<210> 56

<211> 1290

<212> DNA

<213> Human

<400> 56

ATGGAGGGGG AGCCCTCCCA GCCTCCCAAC AGCAGTTGGC CCCTAAGTCA GAATGGGACT 60  
 AACACTGAGG CCACCCCGGC TACAAACCTC ACCTTCTCCT CCTACTATCA GCACACCTCC 120  
 CCTGTGGCGG CCATGTTTCA TGTGGCCTAT GCGCTCATCT TCCTGCTCTG CATGGTGGGC 180  
 AACACCCTGG TCTGTTTTCAT CGTGCTCAAG AACCGGCACA TGCATACTGT CACCAACATG 240  
 TTCATCCTCA ACCTGGCTGT CAGTGACCTG CTGGTGGGCA TCTTCTGCAT GCCCACCACC 300  
 CTTGTGGACA ACCTCATCAC TGGGTGGCCC TTCGACAATG CCACATGCAA GATGAGCGGC 360  
 TTGGTGCAGG GCATGTCTGT GTCGGCTTCC GTTTTCACAC TGGTGGCCAT TGCTGTGGAA 420  
 AGGTTCCGCT GCATCGTGCA CCCTTTCCGC GAGAAGCTGA CCCTGCGGAA GGCCTCGTC 480  
 ACCATCGCCG TCATCTGGGC CCTGGCGCTG CTCATCATGT GTCCCTCGGC CGTCACGCTG 540  
 ACCGTCACCC GTGAGGAGCA CCACTTCATG GTGGACGCCC GCAACCGCTC CTACCCGCTC 600  
 TACTCCTGCT GGGAGGCCTG GCCCGAGAAG GGCATGCGCA GGGTCTACAC CACTGTGCTC 660  
 TTCTCGCACA TCTACCTGGC GCCGCTGGCG CTCATCGTGG TCATGTACGC CCGCATCGCG 720  
 CGCAAGCTCT GCCAGGCCCC GGGCCCGGCC CCCGGGGGCG AGGAGGCTGC GGACCCGCGA 780  
 GCATCGCGGC GCAGAGCGCG CGTGGTGCAC ATGCTGGTCA TGGTGGCGCT GTTCTTCACG 840  
 CTGTCTGGC TGCCGCTCTG GGCCTGCTG CTGCTCATCG ACTACGGGCA GCTCAGCGCG 900  
 CCGCAGCTGC ACCTGGTCAC CGTCTACGCC TTCCCTTCG CGCACTGGCT GGCCTTCTTC 960  
 AACAGCAGCG CCAACCCCAT CATCTACGGC TACTTCAACG AGAACTTCCG CCGCGGCTTC 1020  
 CAGGCCGCCT TCCGCGCCCG CCTCTGCCCC CGCCCGTCGG GGAGCCACAA GGAGGCCTAC 1080  
 TCCGAGCGGC CCGGCGGGCT TCTGCACAGG CGGGTCTTCG TGGTGGTGGC GCCCAGCGAC 1140  
 TCCGGGCTGC CCTCTGAGTC GGGCCCTAGC AGTGGGGCCC CCAGGCCCGG CCGCCTCCCG 1200

CTGCGGAATG GGC GGGTGGC TCACCACGGC TTGCCCAGGG AAGGGCCTGG CTGCTCCCAC 1260

CTGCCCCCTCA CCATTCCAGC CTGGGATATC

1290

<210> 57

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223>

<400> 57

GTCGACATGG AGGGGGAGCC CTCCCAGCCT C

31

<210> 58

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223>

<400> 58

ACTAGTTCAG ATATCCCAGG CTGGAATGG

29



## SEQUENCE LISTING

<110> WATANABE, TAKUYA  
KIKUCHI, KUNIKO  
TERAO, YASUKO  
SHINTANI, YASUSHI  
HINUMA, SHUJI  
FUKUSUMI, SHOJI  
FUJII, RYO  
HOSOYA, MASAKI  
KITADA, CHIEKO

<120> NOVEL G PROTEIN-COUPLED RECEPTOR PROTEIN, ITS DNA AND  
LIGAND THEREOF

<130> 46342-55862

<140> 09/831,758

<141> 2001-05-11

<150> JP 10-323759

<151> 1998-11-13

<150> JP 11-0600030

<151> 1999-03-08

<150> JP 11-106812

<151> 1999-04-14

<150> JP 11-166672

<151> 1999-06-14

<150> JP 11-221640

<151> 1999-08-04

<150> JP 11-259818

<151> 1999-09-14

<160> 63

<170> PatentIn Ver. 2.1

<210> 1

$\langle 211 \rangle$  180

<212> PRT

<213> Homo sapiens

<400> 1

```

<400> 1
Met Glu Ile Ile Ser Ser Lys Leu Phe Ile Leu Leu Thr Leu Ala Thr
      1              5              10              15

```

Ser Ser Leu Leu Thr Ser Asn Ile Phe Cys Ala Asp Glu Leu Val Met  
20 25 30

Ser Asn Leu His Ser Lys Glu Asn Tyr Asp Lys Tyr Ser Glu Pro Arg  
35 40 45

<400>	2															
atg gaa att att tca tca aaa cta ttc att tta ttg act tta gcc act	48															
Met Glu Ile Ile Ser Ser Lys Leu Phe Ile Leu Leu Thr Leu Ala Thr																
1 5 10 15																
tca agc ttg tta aca tca aac att ttt tgt gca gat gaa tta gtg atg	96															
Ser Ser Leu Leu Thr Ser Asn Ile Phe Cys Ala Asp Glu Leu Val Met																
20 25 30																
tcc aat ctt cac agc aaa gaa aat tat gac aaa tat tct gag cct aga	144															
Ser Asn Leu His Ser Lys Glu Asn Tyr Asp Lys Tyr Ser Glu Pro Arg																
35 40 45																
gga tac cca aaa ggg gaa aga agc ctc aat ttt gag gaa tta aaa gat	192															
Gly Tyr Pro Lys Gly Glu Arg Ser Leu Asn Phe Glu Glu Leu Lys Asp																
50 55 60																
tgg gga cca aaa aat gtt att aag atg agt aca cct gca gtc aat aaa	240															
Trp Gly Pro Lys Asn Val Ile Lys Met Ser Thr Pro Ala Val Asn Lys																
65 70 75 80																

atg cca cac tcc ttc gcc aac ttg cca ttg aga ttt ggg agg aac gtt 288  
Met Pro His Ser Phe Ala Asn Leu Pro Leu Arg Phe Gly Arg Asn Val  
85 90 95

caa gaa gaa aga agt gct gga gca aca gcc aac ctg cct ctg aga tct 336  
Gln Glu Glu Arg Ser Ala Gly Ala Thr Ala Asn Leu Pro Leu Arg Ser  
100 105 110

gga aga aat atg gag gtg agc ctc gtg aga cgt gtt cct aac ctg ccc 384  
Gly Arg Asn Met Glu Val Ser Leu Val Arg Arg Val Pro Asn Leu Pro  
115 120 125

caa agg ttt ggg aga aca aca aca gcc aaa agt gtc tgc agg atg ctg 432  
Gln Arg Phe Gly Arg Thr Thr Thr Ala Lys Ser Val Cys Arg Met Leu  
130 135 140

agt gat ttg tgt caa gga tcc atg cat tca cca tgt gcc aat gac tta 480  
Ser Asp Leu Cys Gln Gly Ser Met His Ser Pro Cys Ala Asn Asp Leu  
145 150 155 160

ttt tac tcc atg acc tgc cag cac caa gaa atc cag aat ccc gat caa 528  
Phe Tyr Ser Met Thr Cys Gln His Gln Glu Ile Gln Asn Pro Asp Gln  
165 170 175

aaa cag tca agg taa 543  
Lys Gln Ser Arg  
180

<210> 3  
<211> 27  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 3 27  
gggctgcaca tagagactta atttttag

<210> 4  
<211> 27  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 4 27  
ctagaccacc tctatataac tgcccat

<210> 5  
<211> 30  
<212> DNA  
<213> Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: Primer

&lt;400&gt; 5

gcacatagag acttaatttt agatttagac

30

&lt;210&gt; 6

&lt;211&gt; 27

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: Primer

&lt;400&gt; 6

catgcacttt gactggtttc caggtat

27

&lt;210&gt; 7

&lt;211&gt; 27

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: Primer

&lt;400&gt; 7

cagctttagg gacaggctcc aggtttc

27

&lt;210&gt; 8

&lt;211&gt; 196

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 8

Met	Glu	Ile	Ile	Ser	Ser	Lys	Leu	Phe	Ile	Leu	Leu	Thr	Leu	Ala	Thr
1				5					10					15	

Ser	Ser	Leu	Leu	Thr	Ser	Asn	Ile	Phe	Cys	Ala	Asp	Glu	Leu	Val	Met
		20						25					30		

Ser	Asn	Leu	His	Ser	Lys	Glu	Asn	Tyr	Asp	Lys	Tyr	Ser	Glu	Pro	Arg
	35						40					45			

Gly	Tyr	Pro	Lys	Gly	Glu	Arg	Ser	Leu	Asn	Phe	Glu	Glu	Leu	Lys	Asp
	50					55					60				

Trp	Gly	Pro	Lys	Asn	Val	Ile	Lys	Met	Ser	Thr	Pro	Ala	Val	Asn	Lys
65					70					75				80	

Met	Pro	His	Ser	Phe	Ala	Asn	Leu	Pro	Leu	Arg	Phe	Gly	Arg	Asn	Val
				85					90					95	

Gln	Glu	Glu	Arg	Ser	Ala	Gly	Ala	Thr	Ala	Asn	Leu	Pro	Leu	Arg	Ser
			100					105					110		

Gly Arg Asn Met Glu Val Ser Leu Val Arg Arg Val Pro Asn Leu Pro  
115 120 125

Gln Arg Phe Gly Arg Thr Thr Thr Ala Lys Ser Val Cys Arg Met Leu  
130 135 140

Ser	Asp	Leu	Cys	Gln	Gly	Ser	Met	His	Ser	Pro	Cys	Ala	Asn	Asp	Leu
145					150					155					160

Phe Tyr Ser Met Thr Cys Gln His Gln Glu Ile Gln Asn Pro Asp Gln  
165 170 175

Lys Gln Ser Arg Arg Leu Leu Phe Lys Lys Ile Asp Asp Ala Glu Leu  
180 185 190

Lys Gln Glu Lys  
195

```
<210> 9
<211> 591
<212> DNA
<213> Homo sapiens
```

```
<220>
<221> CDS
<222> (1) .. (588)
```

<400> 9																	
atg	gaa	att	att	tca	tca	aaa	cta	ttc	att	tta	ttg	act	tta	gcc	act	48	
Met	Glu	Ile	Ile	Ser	Ser	Lys	Leu	Phe	Ile	Leu	Leu	Thr	Leu	Ala	Thr		
1				5			10				15						
tca	agc	ttg	tta	aca	tca	aac	att	ttt	tgt	gca	gat	gaa	tta	gtg	atg	96	
Ser	Ser	Leu	Leu	Thr	Ser	Asn	Ile	Phe	Cys	Ala	Asp	Glu	Leu	Val	Met		
20				25				30									
tcc	aat	ctt	cac	agc	aaa	gaa	aat	tat	gac	aaa	tat	tct	gag	cct	aga	144	
Ser	Asn	Leu	His	Ser	Lys	Glu	Asn	Tyr	Asp	Lys	Tyr	Ser	Glu	Pro	Arg		
35				40				45									
gga	tac	cca	aaa	ggg	gaa	aga	agc	ctc	aat	ttt	gag	gaa	tta	aaa	gat	192	
Gly	Tyr	Pro	Lys	Gly	Glu	Arg	Ser	Leu	Asn	Phe	Glu	Glu	Leu	Lys	Asp		
50				55				60									
tgg	gga	cca	aaa	aat	gtt	att	aag	atg	agt	aca	cct	gca	gtc	aat	aaa	240	
Trp	Gly	Pro	Lys	Asn	Val	Ile	Lys	Met	Ser	Thr	Pro	Ala	Val	Asn	Lys		
65				70				75				80					
atg	cca	cac	tcc	ttc	gcc	aac	ttg	cca	ttg	aga	ttt	ggg	agg	aac	gtt	288	
Met	Pro	His	Ser	Phe	Ala	Asn	Leu	Pro	Leu	Arg	Phe	Gly	Arg	Asn	Val		
85				90				95									
caa	gaa	gaa	aga	agt	gct	gga	gca	aca	gcc	aac	ctg	cct	ctg	aga	tct	336	
Gln	Glu	Glu	Arg	Ser	Ala	Gly	Ala	Thr	Ala	Asn	Leu	Pro	Leu	Arg	Ser		
100				105				110									

gga aga aat atg gag gtg agc ctc gtg aga cgt gtt cct aac ctg ccc	384
Gly Arg Asn Met Glu Val Ser Leu Val Arg Arg Val Pro Asn Leu Pro	
115 120 125	
caa agg ttt ggg aga aca aca aca gcc aaa agt gtc tgc agg atg ctg	432
Gln Arg Phe Gly Arg Thr Thr Thr Ala Lys Ser Val Cys Arg Met Leu	
130 135 140	
agt gat ttg tgt caa gga tcc atg cat tca cca tgt gcc aat gac tta	480
Ser Asp Leu Cys Gln Gly Ser Met His Ser Pro Cys Ala Asn Asp Leu	
145 150 155 160	
ttt tac tcc atg acc tgc cag cac caa gaa atc cag aat ccc gat caa	528
Phe Tyr Ser Met Thr Cys Gln His Gln Glu Ile Gln Asn Pro Asp Gln	
165 170 175	
aaa cag tca agg aga ctg cta ttc aag aaa ata gat gat gca gaa ttg	576
Lys Gln Ser Arg Arg Leu Leu Phe Lys Lys Ile Asp Asp Ala Glu Leu	
180 185 190	
aaa caa gaa aaa taa	591
Lys Gln Glu Lys	
195	

<210> 10  
 <211> 27  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer

<400> 10	
gcctagagga gatctaggct gggagga	27

<210> 11  
 <211> 27  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer

<400> 11	
gggaggaaca tggaagaaga aaggagc	27

<210> 12  
 <211> 27  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer

27

```
<210> 13
<211> 27
<212> DNA
<213> Artificial Sequence
```

<220>  
<223> Description of Artificial Sequence: Primer

27

```
<210> 14
<211> 196
<212> PRT
<213> Bos sp.
```

<400> 14																	
Met	Glu	Ile	Ile	Ser	Leu	Lys	Arg	Phe	Ile	Leu	Leu	Met	Leu	Ala	Thr		
1				5					10					15			
Ser	Ser	Leu	Leu	Thr	Ser	Asn	Ile	Phe	Cys	Thr	Asp	Glu	Ser	Arg	Met		
			20					25					30				
Pro	Asn	Leu	Tyr	Ser	Lys	Lys	Asn	Tyr	Asp	Lys	Tyr	Ser	Glu	Pro	Arg		
		35					40					45					
Gly	Asp	Leu	Gly	Trp	Glu	Lys	Glu	Arg	Ser	Leu	Thr	Phe	Glu	Glu	Val		
	50					55					60						
Lys	Asp	Trp	Ala	Pro	Lys	Ile	Lys	Met	Asn	Lys	Pro	Val	Val	Asn	Lys		
65					70					75					80		
Met	Pro	Pro	Ser	Ala	Ala	Asn	Leu	Pro	Leu	Arg	Phe	Gly	Arg	Asn	Met		
				85					90					95			
Glu	Glu	Glu	Arg	Ser	Thr	Arg	Ala	Met	Ala	His	Leu	Pro	Leu	Arg	Leu		
			100					105					110				
Gly	Lys	Asn	Arg	Glu	Asp	Ser	Leu	Ser	Arg	Trp	Val	Pro	Asn	Leu	Pro		
		115					120					125					
Gln	Arg	Phe	Gly	Arg	Thr	Thr	Thr	Ala	Lys	Ser	Ile	Thr	Lys	Thr	Leu		
	130					135					140						
Ser	Asn	Leu	Leu	Gln	Gln	Ser	Met	His	Ser	Pro	Ser	Thr	Asn	Gly	Leu		
145				150						155					160		
Leu	Tyr	Ser	Met	Ala	Cys	Gln	Pro	Gln	Glu	Ile	Gln	Asn	Pro	Gly	Gln		
				165					170					175			
Lys	Asn	Leu	Arg	Arg	Arg	Gly	Phe	Gln	Lys	Ile	Asp	Asp	Ala	Glu	Leu		
			180					185					190				

<400> 15																	
atg	gaa	att	att	tca	tta	aaa	cga	ttc	att	tta	ttg	atg	tta	gcc	act	48	
Met	Glu	Ile	Ile	Ser	Leu	Lys	Arg	Phe	Ile	Leu	Leu	Met	Leu	Ala	Thr		
1				5				10						15			
tca	agc	ttg	tta	aca	tca	aac	atc	ttc	tgc	aca	gac	gaa	tca	agg	atg	96	
Ser	Ser	Leu	Leu	Thr	Ser	Asn	Ile	Phe	Cys	Thr	Asp	Glu	Ser	Arg	Met		
		20						25						30			
ccc	aat	ctt	tac	agc	aaa	aag	aat	tat	gac	aaa	tat	tcc	gag	cct	aga	144	
Pro	Asn	Leu	Tyr	Ser	Lys	Lys	Asn	Tyr	Asp	Lys	Tyr	Ser	Glu	Pro	Arg		
		35				40						45					
gga	gat	cta	ggc	tgg	gag	aaa	gaa	aga	agt	ctt	act	ttt	gaa	gaa	gta	192	
Gly	Asp	Leu	Gly	Trp	Glu	Lys	Glu	Arg	Ser	Leu	Thr	Phe	Glu	Glu	Val		
50						55						60					
aaa	gat	tgg	gct	cca	aaa	att	aag	atg	aat	aaa	cct	gta	gtc	aac	aaa	240	
Lys	Asp	Trp	Ala	Pro	Lys	Ile	Lys	Met	Asn	Lys	Pro	Val	Val	Asn	Lys		
65						70						75		80			
atg	cca	cct	tct	gca	gcc	aac	ctg	cca	ctg	aga	ttt	ggg	agg	aac	atg	288	
Met	Pro	Pro	Ser	Ala	Ala	Asn	Leu	Pro	Leu	Arg	Phe	Gly	Arg	Asn	Met		
				85						90				95			
gaa	gaa	gaa	agg	agc	act	agg	gcg	atg	gcc	cac	ctg	cct	ctg	aga	ctc	336	
Glu	Glu	Glu	Arg	Ser	Thr	Arg	Ala	Met	Ala	His	Leu	Pro	Leu	Arg	Leu		
		100						105						110			
gga	aaa	aat	aga	gag	gac	agc	ctc	tcc	aga	tgg	gtc	cca	aat	ctg	ccc	384	
Gly	Lys	Asn	Arg	Glu	Asp	Ser	Leu	Ser	Arg	Trp	Val	Pro	Asn	Leu	Pro		
		115				120						125					
cag	agg	ttt	gga	aga	aca	aca	aca	gcc	aaa	agc	att	acc	aag	acc	ctg	432	
Gln	Arg	Phe	Gly	Arg	Thr	Thr	Thr	Ala	Lys	Ser	Ile	Thr	Lys	Thr	Leu		
130						135						140					
agt	aat	ttg	ctc	cag	cag	tcc	atg	cat	tca	cca	tct	acc	aat	ggg	cta	480	
Ser	Asn	Leu	Leu	Gln	Gln	Ser	Met	His	Ser	Pro	Ser	Thr	Asn	Gly	Leu		
145				150						155				160			
ctc	tac	tcc	atg	gcc	tgc	cag	ccc	caa	gaa	atc	cag	aat	cct	ggg	caa	528	
Leu	Tyr	Ser	Met	Ala	Cys	Gln	Pro	Gln	Glu	Ile	Gln	Asn	Pro	Gly	Gln		
				165						170				175			



aaa caa gaa aaa taa 591  
Lys Gln Glu Lys  
195

Asn Lys Val Pro His Ser Ala Ala Asn Leu Pro Leu Arg Phe Gly Arg  
85 90 95

[illegible]

aac ata gaa gac aga aga agc ccc agg gca cgg gcc aac atg gag gca 336  
 Asn Ile Glu Asp Arg Arg Ser Pro Arg Ala Arg Ala Asn Met Glu Ala  
 100 105 110

ggg acc atg agc cat ttt ccc agc ctg ccc caa agg ttt ggg aga aca 384  
 Gly Thr Met Ser His Phe Pro Ser Leu Pro Gln Arg Phe Gly Arg Thr  
 115 120 125

aca gcc aga cgc atc acc aag aca ctg gct ggt ttg ccc cag aaa tcc 432  
 Thr Ala Arg Arg Ile Thr Lys Thr Leu Ala Gly Leu Pro Gln Lys Ser  
 130 135 140

ctg cac tcc ctg gcc tcc agt gaa tcg ctc tat gcc atg acc cgc cag 480  
 Leu His Ser Leu Ala Ser Ser Glu Ser Leu Tyr Ala Met Thr Arg Gln  
 145 150 155 160

cat caa gaa att cag agt cct ggt caa gag caa cct agg aaa cgg gtg 528  
 His Gln Glu Ile Gln Ser Pro Gly Gln Glu Gln Pro Arg Lys Arg Val  
 165 170 175

ttc acg gaa aca gat gat gca gaa agg aaa caa gaa aaa ata gga aac 576  
 Phe Thr Glu Thr Asp Asp Ala Glu Arg Lys Gln Glu Lys Ile Gly Asn  
 180 185 190

ctc cag cca gtc ctt caa ggg gct atg aag ctg tga 612  
 Leu Gln Pro Val Leu Gln Gly Ala Met Lys Leu  
 195 200

<210> 20  
 <211> 12  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Probe

<220>  
 <221> modified\_base  
 <222> (9)  
 <223> a, c, t, g, other or unknown

<400> 20  
 mgnttyggna ar

12

<210> 21  
 <211> 12  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Probe

<220>  
 <221> modified\_base  
 <222> (3)  
 <223> a, c, t, g, other or unknown

<220>  
 <221> modified\_base  
 <222> (9)  
 <223> a, c, t, g, other or unknown

<220>  
 <221> modified\_base  
 <222> (12)  
 <223> a, c, t, g, other or unknown

<400> 21  
 mgnttyggnm gn

12

<210> 22  
 <211> 12  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Probe

<220>  
 <221> modified\_base  
 <222> (3)  
 <223> a, c, t, g, other or unknown

<220>  
 <221> modified\_base  
 <222> (6)  
 <223> a, c, t, g, other or unknown

<220>  
 <221> modified\_base  
 <222> (9)  
 <223> a, c, t, g, other or unknown

<400> 22  
 mgnwsnggna ar

12

<210> 23  
 <211> 12  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Probe

<220>  
 <221> modified\_base  
 <222> (3)  
 <223> a, c, t, g, other or unknown

<220>  
 <221> modified\_base







Pro His Phe His Ser Lys Glu Gly Asp Gly Lys Tyr Ser Gln Leu Arg  
35 40 45  
Gly Ile Pro Lys Gly Glu Lys Glu Arg Ser Val Ser Phe Gln Glu Leu  
50 55 60  
Lys Asp Trp Gly Ala Lys Asn Val Ile Lys Met Ser Pro Ala Pro Ala  
65 70 75 80  
Asn Lys Val Pro His Ser Ala Ala Asn Leu Pro Leu Arg Phe Gly Arg  
85 90 95  
Thr Ile Asp Glu Lys Arg Ser Pro Ala Ala Arg Val Asn Met Glu Ala  
100 105 110  
Gly Thr Arg Ser His Phe Pro Ser Leu Pro Gln Arg Phe Gly Arg Thr  
115 120 125  
Thr Ala Arg Ser Pro Lys Thr Pro Ala Asp Leu Pro Gln Lys Pro Leu  
130 135 140  
His Ser Leu Gly Ser Ser Glu Leu Leu Tyr Val Met Ile Cys Gln His  
145 150 155 160  
Gln Glu Ile Gln Ser Pro Gly Gly Lys Arg Thr Arg Arg Gly Ala Phe  
165 170 175  
Val Glu Thr Asp Asp Ala Glu Arg Lys Pro Glu Lys  
180 185

<210> 34  
<211> 618  
<212> DNA  
<213> Mus sp.

<220>  
<221> CDS  
<222> (17)..(580)

<400> 34  
tttagactta gacgaa atg gaa att att tca tta aaa cga ttc att tta ttg 52  
Met Glu Ile Ile Ser Leu Lys Arg Phe Ile Leu Leu  
1 5 10  
act gtg gca act tca agc ttc tta aca tca aac acc ttc tgt aca gat 100  
Thr Val Ala Thr Ser Ser Phe Leu Thr Ser Asn Thr Phe Cys Thr Asp  
15 20 25  
gag ttc atg atg cct cat ttt cac agc aaa gaa ggt gac gga aaa tac 148  
Glu Phe Met Met Pro His Phe His Ser Lys Glu Gly Asp Gly Lys Tyr  
30 35 40  
tcc cag ctg aga gga atc cca aaa ggg gaa aag gaa aga agt gtc agt 196  
Ser Gln Leu Arg Gly Ile Pro Lys Gly Glu Lys Glu Arg Ser Val Ser  
45 50 55 60



ttt	caa	gaa	cta	aaa	gat	tgg	ggg	gca	aag	aat	gtt	att	aag	atg	agt		244
Phe	Gln	Glu	Leu	Lys	Asp	Trp	Gly	Ala	Lys	Asn	Val	Ile	Lys	Met	Ser		
				65					70					75			
cca	gcc	cct	gcc	aac	aaa	gtg	ccc	cac	tca	gca	gcc	aac	ctg	ccc	ctg		292
Pro	Ala	Pro	Ala	Asn	Lys	Val	Pro	His	Ser	Ala	Ala	Asn	Leu	Pro	Leu		
			80					85					90				
aga	ttt	gga	agg	acc	ata	gat	gag	aaa	aga	agc	ccc	gca	gca	cgg	gtc		340
Arg	Phe	Gly	Arg	Thr	Ile	Asp	Glu	Lys	Arg	Ser	Pro	Ala	Ala	Arg	Val		
		95					100					105					
aac	atg	gag	gca	ggg	acc	agg	agc	cat	ttc	ccc	agc	ctg	ccc	caa	agg		388
Asn	Met	Glu	Ala	Gly	Thr	Arg	Ser	His	Phe	Pro	Ser	Leu	Pro	Gln	Arg		
	110					115					120						
ttt	ggg	aga	aca	aca	gcc	aga	agc	ccc	aag	aca	ccc	gct	gat	ttg	cca		436
Phe	Gly	Arg	Thr	Thr	Ala	Arg	Ser	Pro	Lys	Thr	Pro	Ala	Asp	Leu	Pro		
125					130					135					140		
cag	aaa	ccc	ctg	cac	tca	ctg	ggc	tcc	agc	gag	ttg	ctc	tac	gtc	atg		484
Gln	Lys	Pro	Leu	His	Ser	Leu	Gly	Ser	Ser	Glu	Leu	Leu	Tyr	Val	Met		
				145				150						155			
atc	tgc	cag	cac	caa	gaa	att	cag	agt	cct	ggc	gga	aag	cga	acg	agg		532
Ile	Cys	Gln	His	Gln	Glu	Ile	Gln	Ser	Pro	Gly	Gly	Lys	Arg	Thr	Arg		
			160					165					170				
aga	gga	gcg	ttt	gtg	gaa	aca	gat	gat	gca	gaa	agg	aaa	cca	gaa	aaa		580
Arg	Gly	Ala	Phe	Val	Glu	Thr	Asp	Asp	Ala	Glu	Arg	Lys	Pro	Glu	Lys		
			175				180					185					
tag	gaa	aac	ct	cgag	cccc	gac	ttca	agaggc	tac	ggagc							618

```
<210> 35
<211> 27
<212> DNA
<213> Artificial Sequence
```

<220>  
<223> Description of Artificial Sequence: Primer

```
<400> 35
agtcgacagt atggaggcgg agccctc
```

```
<210> 36
<211> 29
<212> DNA
<213> Artificial Sequence
```

<220>  
<223> Description of Artificial Sequence: Primer

<400> 36  
gactagttca aatgttccag gccgggatg 29



Met Leu Val Met Val Ala Leu Phe Phe Thr Leu Ser Trp Leu Pro Leu  
275 280 285

Trp Val Leu Leu Leu Leu Ile Asp Tyr Gly Glu Leu Ser Glu Leu Gln  
290 295 300

Leu His Leu Leu Ser Val Tyr Ala Phe Pro Leu Ala His Trp Leu Ala  
305 310 315 320

Phe Phe His Ser Ser Ala Asn Pro Ile Ile Tyr Gly Tyr Phe Asn Glu  
325 330 335

Asn Phe Arg Arg Gly Phe Gln Ala Ala Phe Arg Ala Gln Leu Cys Trp  
340 345 350

Pro Pro Trp Ala Ala His Lys Gln Ala Tyr Ser Glu Arg Pro Asn Arg  
355 360 365

Leu Leu Arg Arg Arg Val Val Val Asp Val Gln Pro Ser Asp Ser Gly  
370 375 380

Leu Pro Ser Glu Ser Gly Pro Ser Ser Gly Val Pro Gly Pro Gly Arg  
385 390 395 400

Leu Pro Leu Arg Asn Gly Arg Val Ala His Gln Asp Gly Pro Gly Glu  
405 410 415

Gly Pro Gly Cys Asn His Met Pro Leu Thr Ile Pro Ala Trp Asn Ile  
420 425 430

<210> 38

<211> 1299

<212> DNA

<213> Rattus sp.

<400> 38

2400> 38							
atggaggcgg	agccctccca	gcctcccaac	ggcagctggc	ccctgggtca	gaacgggagt	60	
gatgtggaga	ccagcatggc	aaccagcctc	accttctcct	cctaactacca	acactcctct	120	
ccggtggcag	ccatgttcat	cgcggcctac	gtgctcatct	tctctctctg	catggtgggc	180	
aacaccctgg	tctgcttcat	tgtgctcaag	aaccggcaca	tgcgcactgt	caccaacatg	240	
tttatcctca	acctggccgt	cagcgacctg	ctggtgggca	tcttctgcat	gcccacaacc	300	
cttgtggaca	accttatcac	tggttggcct	tttgacaacg	ccacatgcaa	gatgagcggc	360	
ttggtgcagg	gcatgtccgt	gtctgcatcg	gttttccacac	tggtggccat	cgctgtggaa	420	
aggttccgct	gcatcgtgca	ccctttccgc	gagaagctga	cccttcggaa	ggcgctgttc	480	
accatcgcg	tgatctgggc	tctggcgctg	ctcatcatgt	gtccctcggc	ggctactctg	540	
acagtcaccc	gagaggagca	tcatctcatg	ctggatgctc	gtaaccgctc	ctacccgctc	600	
tactcgtgct	gggaggcctg	gcccgagaag	ggcatgcgca	aggtctacac	cgcggtgctc	660	
ttcgcgcaca	tctacctgg	gccgctggcg	ctcatcgtag	tgatgtacgt	gcgcatcgcg	720	
cgcaagctat	gccaggcccc	cggctcctgcg	cgcgacacgg	aggaggcgg	ggccgagggt	780	
ggccgcactt	cgcgcctgtag	ggcccgcgtg	gtgcacatgc	tggtcatggt	ggcgctcttc	840	
ttcacgttgt	cctggctgcc	actctgggtg	ctgctgctgc	tcatcgacta	tggggagctg	900	
agcgagctgc	aactgcacct	gctgtcggtc	tacgccttcc	ccttggcaca	ctggctggcc	960	
ttctttccaca	gcagcgccaa	ccccatcatc	tacggctact	tcaacgagaa	cttcgcgcgc	1020	
ggcttccagg	ctgccttcgg	tgcacagctc	tgctggcctc	cctgggccgc	ccacaagcaa	1080	
gcctactcgg	agcgcccaa	ccgcctcctg	cgcaggcggg	tgggtgggga	cgtgcaaccc	1140	
agcgactcgg	gcctgccatc	agagtctggc	cccagcagcg	gggtcccagg	gcctggccgg	1200	
ctgccactgc	gcaatgggcg	tgtggcccat	caggatggcc	cgggggaagg	gccaggctgc	1260	

aaccacatgc ccctcaccat cccggcctgg aacatttga

1299

<210> 39  
 <211> 12  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic peptide

<400> 39  
 Met Pro His Ser Phe Ala Asn Leu Pro Leu Arg Phe  
 1 5 10

<210> 40  
 <211> 8  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic peptide

<400> 40  
 Val Pro Asn Leu Pro Gln Arg Phe  
 1 5

<210> 41  
 <211> 11  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic peptide

<400> 41  
 Ser Ala Gly Ala Thr Ala Asn Leu Pro Arg Ser  
 1 5 10

<210> 42  
 <211> 36  
 <212> DNA  
 <213> Homo sapiens

<400> 42  
 atgccacact ccttcgccaa cttgccattg agattt

36

<210> 43  
 <211> 36  
 <212> DNA  
 <213> Homo sapiens

<400> 43  
agtgctggag caacagccaa cctgcctctg agatct 36

<210> 44  
<211> 24  
<212> DNA  
<213> Homo sapiens

<400> 44  
gttcctaacc tgcccaaaag gttt 24

<210> 45  
<211> 276  
<212> DNA  
<213> Homo sapiens

<400> 45  
atggaaatta tttcatcaaa actattcatt ttattgactt tagccacttc aagcttggtta 60  
acatcaaaca ttttttgtgc agatgaatta gtgatgtcca atcttcacag caaagaaaat 120  
tatgacaaat attctgagcc tagaggatac ccaaaagggg aaagaagcct caattttgag 180  
gaattaaaag attggggacc aaaaaatggtt attaagatga gtacacctgc agtcaataaa 240  
atgccacact ccttcgccaa cttgccattg agattt 276

<210> 46  
<211> 336  
<212> DNA  
<213> Homo sapiens

<400> 46  
atggaaatta tttcatcaaa actattcatt ttattgactt tagccacttc aagcttggtta 60  
acatcaaaca ttttttgtgc agatgaatta gtgatgtcca atcttcacag caaagaaaat 120  
tatgacaaat attctgagcc tagaggatac ccaaaagggg aaagaagcct caattttgag 180  
gaattaaaag attggggacc aaaaaatggtt attaagatga gtacacctgc agtcaataaa 240  
atgccacact ccttcgccaa cttgccattg agatttggga ggaacgttca agaagaaaga 300  
agtgctggag caacagccaa cctgcctctg agatct 336

<210> 47  
<211> 393  
<212> DNA  
<213> Homo sapiens

<400> 47  
atggaaatta tttcatcaaa actattcatt ttattgactt tagccacttc aagcttggtta 60  
acatcaaaca ttttttgtgc agatgaatta gtgatgtcca atcttcacag caaagaaaat 120  
tatgacaaat attctgagcc tagaggatac ccaaaagggg aaagaagcct caattttgag 180  
gaattaaaag attggggacc aaaaaatggtt attaagatga gtacacctgc agtcaataaa 240  
atgccacact ccttcgccaa cttgccattg agatttggga ggaacgttca agaagaaaga 300  
agtgctggag caacagccaa cctgcctctg agatctggaa gaaatatgga ggtgagcctc 360  
gtgagacgtg ttctaactt gccccaaagg ttt 393

<210> 48  
<211> 27

<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 48  
ccctggggct tcttctgtct tctatgt

27

<210> 49  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 49  
agcgattcat tttattgact ttagca

26

<210> 50  
<211> 203  
<212> PRT  
<213> Rattus sp.

<400> 50  
Met Glu Ile Ile Ser Ser Lys Arg Phe Ile Leu Leu Thr Leu Ala Thr  
1 5 10 15  
Ser Ser Phe Leu Thr Ser Asn Thr Leu Cys Ser Asp Glu Leu Met Met  
20 25 30  
Pro His Phe His Ser Lys Glu Gly Tyr Gly Lys Tyr Tyr Gln Leu Arg  
35 40 45  
Gly Ile Pro Lys Gly Val Lys Glu Arg Ser Val Thr Phe Gln Glu Leu  
50 55 60  
Lys Asp Trp Gly Ala Lys Lys Asp Ile Lys Met Ser Pro Ala Pro Ala  
65 70 75 80  
Asn Lys Val Pro His Ser Ala Ala Asn Leu Pro Leu Arg Phe Gly Arg  
85 90 95  
Asn Ile Glu Asp Arg Arg Ser Pro Arg Ala Arg Ala Asn Met Glu Ala  
100 105 110  
Gly Thr Met Ser His Phe Pro Ser Leu Pro Gln Arg Phe Gly Arg Thr  
115 120 125  
Thr Ala Arg Arg Ile Thr Lys Thr Leu Ala Gly Leu Pro Gln Lys Ser  
130 135 140  
Leu His Ser Leu Ala Ser Ser Glu Leu Leu Tyr Ala Met Thr Arg Gln  
145 150 155 160

His Gln Glu Ile Gln Ser Pro Gly Gln Glu Gln Pro Arg Lys Arg Val  
 165 170 175

Phe Thr Glu Thr Asp Asp Ala Glu Arg Lys Gln Glu Lys Ile Gly Asn  
 180 185 190

Leu Gln Pro Val Leu Gln Gly Ala Met Lys Leu  
 195 200

<210> 51  
 <211> 609  
 <212> DNA  
 <213> Rattus sp.

<400> 51  
 atggaaatta tttcatcaaa gcgattcatt ttattgactt tagcaacttc aagctttctta 60  
 acttcaaaca ccctttgttc agatgaatta atgatgcccc attttcacag caaagaaggt 120  
 tatggaaaat attaccagct gagaggaatc ccaaaagggg taaaggaaaag aagtgtcact 180  
 tttcaagaac tcaaagattg gggggcaaag aaagatatta agatgagtcc agcccctgcc 240  
 aacaaagtgc ccactcagc agccaacctt cccctgaggt ttgggaggaa catagaagac 300  
 agaagaagcc ccagggcacg ggccaacatg gaggcaggga ccatgagcca ttttcccagc 360  
 ctgccccaaa ggtttgggag aacaacagcc agacgcatca ccaagacact ggctgggttg 420  
 cccagaaat ccctgcactc cctggcctcc agtgaattgc tctatgccat gaccgcccag 480  
 catcaagaaa ttcagagtcc tggtaagag caacctagga aacgggtgtt cacggaaaca 540  
 gatgatgcag aaaggaaaca agaaaaata ggaaacctcc agccagtcct tcaaggggct 600  
 atgaagctg 609

<210> 52  
 <211> 27  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer

<400> 52  
 ttctagattt tggacaaaat ggaaatt 27

<210> 53  
 <211> 27  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer

<400> 53  
 cgtctttagg gacaggctcc agatttc 27

<210> 54  
 <211> 430  
 <212> PRT  
 <213> Homo sapiens

<400> 54

Met Glu Gly Glu Pro Ser Gln Pro Pro Asn Ser Ser Trp Pro Leu Ser  
1 5 10 15

Gln Asn Gly Thr Asn Thr Glu Ala Thr Pro Ala Thr Asn Leu Thr Phe  
20 25 30

Ser Ser Tyr Tyr Gln His Thr Ser Pro Val Ala Ala Met Phe Ile Val  
35 40 45

Ala Tyr Ala Leu Ile Phe Leu Leu Cys Met Val Gly Asn Thr Leu Val  
50 55 60

Cys Phe Ile Val Leu Lys Asn Arg His Met His Thr Val Thr Asn Met  
65 70 75 80

Phe Ile Leu Asn Leu Ala Val Ser Asp Leu Leu Val Gly Ile Phe Cys  
85 90 95

Met Pro Thr Thr Leu Val Asp Asn Leu Ile Thr Gly Trp Pro Phe Asp  
100 105 110

Asn Ala Thr Cys Lys Met Ser Gly Leu Val Gln Gly Met Ser Val Ser  
115 120 125

Ala Ser Val Phe Thr Leu Val Ala Ile Ala Val Glu Arg Phe Arg Cys  
130 135 140

Ile Val His Pro Phe Arg Glu Lys Leu Thr Leu Arg Lys Ala Leu Val  
145 150 155 160

Thr Ile Ala Val Ile Trp Ala Leu Ala Leu Leu Ile Met Cys Pro Ser  
165 170 175

Ala Val Thr Leu Thr Val Thr Arg Glu Glu His His Phe Met Val Asp  
180 185 190

Ala Arg Asn Arg Ser Tyr Pro Leu Tyr Ser Cys Trp Glu Ala Trp Pro  
195 200 205

Glu Lys Gly Met Arg Arg Val Tyr Thr Thr Val Leu Phe Ser His Ile  
210 215 220

Tyr Leu Ala Pro Leu Ala Leu Ile Val Val Met Tyr Ala Arg Ile Ala  
225 230 235 240

Arg Lys Leu Cys Gln Ala Pro Gly Pro Ala Pro Gly Gly Glu Glu Ala  
245 250 255

Ala Asp Pro Arg Ala Ser Arg Arg Arg Ala Arg Val Val His Met Leu  
260 265 270

Val Met Val Ala Leu Phe Phe Thr Leu Ser Trp Leu Pro Leu Trp Ala  
275 280 285

Leu Leu Leu Leu Ile Asp Tyr Gly Gln Leu Ser Ala Pro Gln Leu His  
290 295 300



Leu Val Thr Val Tyr Ala Phe Pro Phe Ala His Trp Leu Ala Phe Phe  
305 310 315 320

Asn Ser Ser Ala Asn Pro Ile Ile Tyr Gly Tyr Phe Asn Glu Asn Phe  
325 330 335

Arg Arg Gly Phe Gln Ala Ala Phe Arg Ala Arg Leu Cys Pro Arg Pro  
340 345 350

Ser Gly Ser His Lys Glu Ala Tyr Ser Glu Arg Pro Gly Gly Leu Leu  
355 360 365

His Arg Arg Val Phe Val Val Val Arg Pro Ser Asp Ser Gly Leu Pro  
370 375 380

Ser Glu Ser Gly Pro Ser Ser Gly Ala Pro Arg Pro Gly Arg Leu Pro  
385 390 395 400

Leu Arg Asn Gly Arg Val Ala His His Gly Leu Pro Arg Glu Gly Pro  
405 410 415

Gly Cys Ser His Leu Pro Leu Thr Ile Pro Ala Trp Asp Ile  
420 425 430

<210> 55  
<211> 1290  
<212> DNA  
<213> Homo sapiens

<400> 55  
atggaggggg agccctccca gcctcccaac agcagttggc ccctaagtca gaatgggact 60  
aacactgagg ccaccccggc tacaaacctc accttctcct cctactatca gcacacctcc 120  
cctgtggcgg ccatgttcat tgtggcctat gcgctcatct tctgtcttg catgggtgggc 180  
aacaccttgg tctgtttcat cgtgtctcaag aaccggcaca tgcatactgt caccaacatg 240  
ttcatcctca acctggctgt cagtgcctg ctgggtgggca tcttctgcat gccaccacc 300  
cttgtggaca acctcatcac tgggtggccc ttcgacaatg ccacatgcaa gatgagcggc 360  
ttggtgcagg gcatgtctgt gtcggcttcc gttttcacac tgggtggccat tgctgtggaa 420  
aggttccgct gcatcgtgca ccctttccgc gagaagctga ccctgcggaa ggcgctcgtc 480  
accatcgccg tcatctgggc cctggcgctg ctcatcatgt gtccctcggc cgtcacgctg 540  
accgtcaccg gtgaggagca ccacttcatt gtggacgccc gcaaccgctc ctaccctctc 600  
tactcctgct gggaggcctg gcccgagaag ggcattgcga ggggtctacac cactgtgctc 660  
ttctcgcaca tctacctggc gccgctggcg ctcactgtgg tcatgtacgc ccgcatcgcg 720  
cgcaagctct gccagggccc gggcccgccc cccggggggcg aggaggctgc ggaccgcga 780  
gcatcgcggc gcagagcgcg cgtgggtgcac atgctggtca tgggtggcgct gttcttcacg 840  
ctgtcctggc tgccgctctg ggcgctgctg ctgctcatcg actacgggca gctcagcgcg 900  
ccgcagctgc acctggtcac cgtctacgcc ttccccctcg cgcactggct ggccttcttc 960  
aacagcagcg ccaaccccat catctacggc tacttcaacg agaacttccg ccgcggttcc 1020  
caggccgctt tccgcgccc cctctgccc cgcccgctcg ggagccacaa ggaggcctac 1080  
tccgagcggc ccggcgggct tctgcacagg cgggtcttcg tgggtggcg gcccagcgac 1140  
tccgggctgc cctctgagtc gggccctagc agtggggccc ccaggcccgg ccgcctccc 1200  
ctgcggaatg ggcggtggc tcaccacggc ttgcccaggg aagggcctgg ctgctcccac 1260  
ctgcccctca ccattccagc ctgggatata 1290

<210> 56  
<211> 1290

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 56

```

atggagggggg agccctccca gcctcccaac agcagttggc ccctaagtca gaatgggact 60
aacactgagg ccaccccggc taaaaacctc accttctcct cctactatca gcacacctcc 120
cctgtggcgg ccattgttcat tgtggcctat gcgctcatct tcctgctctg catgggtggc 180
aacaccctgg tctgtttcat cgtgctcaag aaccggcaca tgcatactgt caccaacatg 240
ttcatcctca acctggctgt cagtgcctg ctgggtgggca tcttctgcat gcccaccacc 300
cttgtggaca acctcatcac tgggtggccc ttcgacaatg ccacatgcaa gatgagcggc 360
ttgggtgcagg gcatgtctgt gtcggcttcc gttttcacac tgggtggccat tgctgtggaa 420
aggttccgct gcatcgtgca ccctttccgc gagaagctga ccctgcggaa ggcgctcgtc 480
accatcgccg tcactctgggc cctggcgctg ctcatcatgt gtccctcggc cgtcacgctg 540
accgtcaccg gtgaggagca ccacttcacg gtggacgccc gcaaccgctc ctaccgctc 600
tactcctgct gggaggcctg gcccgagaag ggcacgcgca ggggtctacac cactgtgctc 660
ttctcgcaca tctacctggc gccgctggcg ctcatcgtgg tcatgtacgc ccgcatcgcg 720
cgcaagctct gccaggcccc gggcccgccc cccggggcgagg agggagctgc ggacccgcga 780
gcatcgcggc gcagagcgcg cgtgggtgcac atgctgggtca tgggtggcgt gttcttcacg 840
ctgtcctggc tgccgctctg ggcgctgctg ctgctcatcg actacgggca gctcagcgcg 900
ccgcagctgc acctggtcac cgtctacgcc ttcccctcg cgcactggct ggccttcttc 960
aacagcagcg ccaaccccat catctacggc tacttcaacg agaacttccg ccgcgggcttc 1020
caggccgcct tccgcgccc cctctgccc cgcccgtcgg ggagccacaa ggaggcctac 1080
tccgagcggc ccggcgggct tctgcacagg cgggtcttcg tgggtgggtgc gcccagcgac 1140
tccgggctgc cctctgagtc gggccctagc agtggggccc ccaggcccgg ccgcctccc 1200
ctgcggaatg ggcgggtggc tcaccacggc ttgccaggg aagggcctgg ctgctccac 1260
ctgccccca ccattccagc ctgggatata 1290

```

&lt;210&gt; 57

&lt;211&gt; 31

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: Primer

31

&lt;400&gt; 57

gtcgacatgg agggggagcc ctcccagcct c

&lt;210&gt; 58

&lt;211&gt; 29

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: Primer

29

&lt;400&gt; 58

actagttcag atatcccagg ctggaatgg

&lt;210&gt; 59

&lt;211&gt; 4

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 59

Phe Met Arg Phe

1

<210> 60

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 60

Leu Pro Leu Arg Phe

1

5

<210> 61

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 61

Leu Pro Leu Arg Ser

1

5

<210> 62

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 62

Leu Pro Gln Arg Phe

1

5

<210> 63

<211> 5

<212> PRT

<213> Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
peptide

&lt;400&gt; 63

Leu Pro Leu Arg Leu

1

5